

FIG. 1A

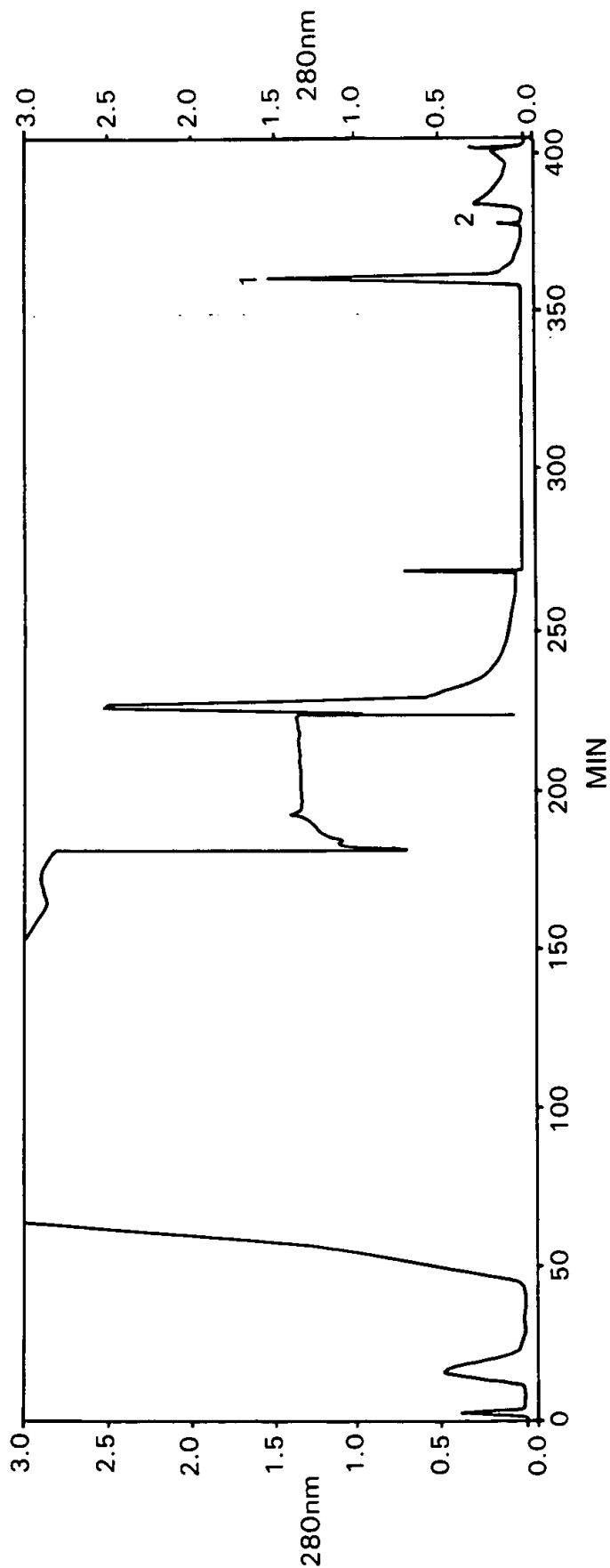


FIG. 1B

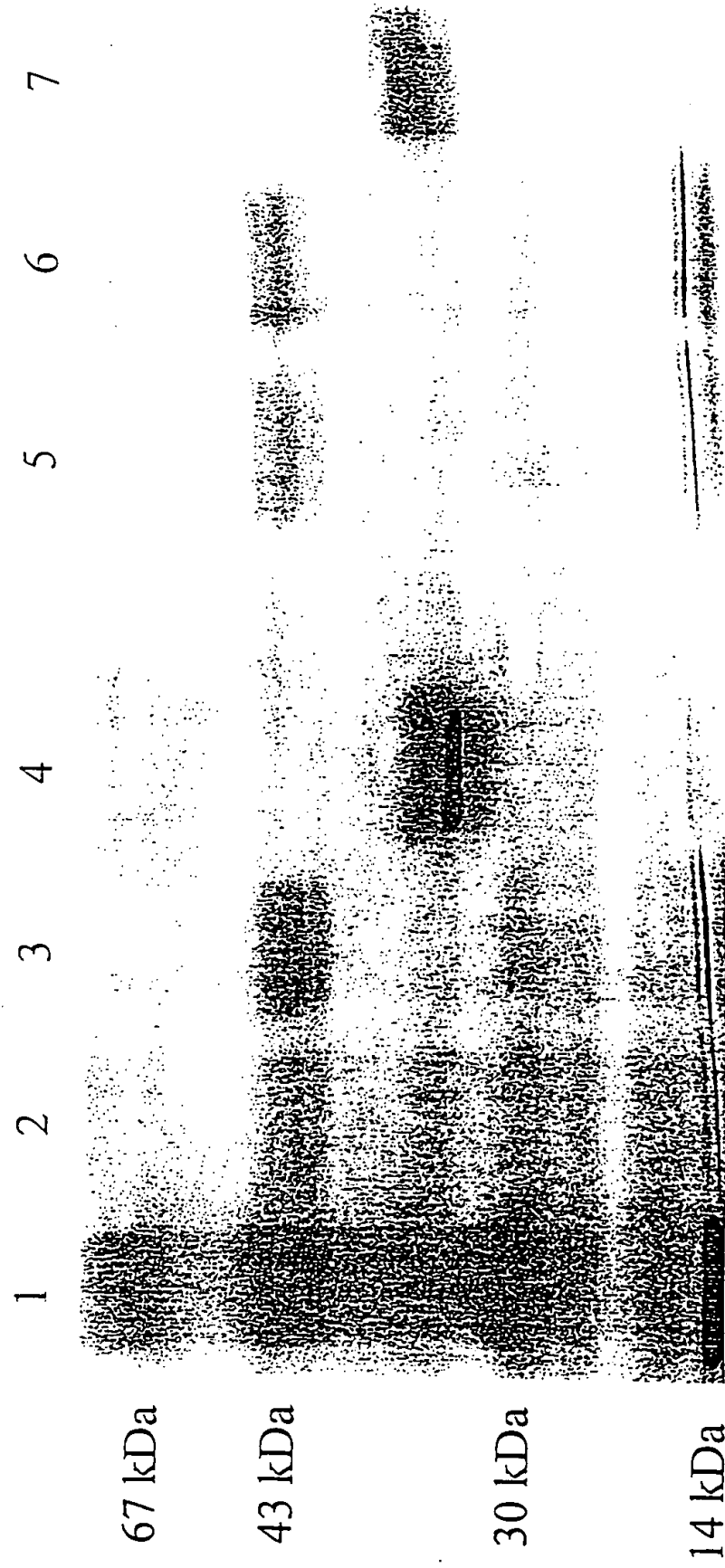
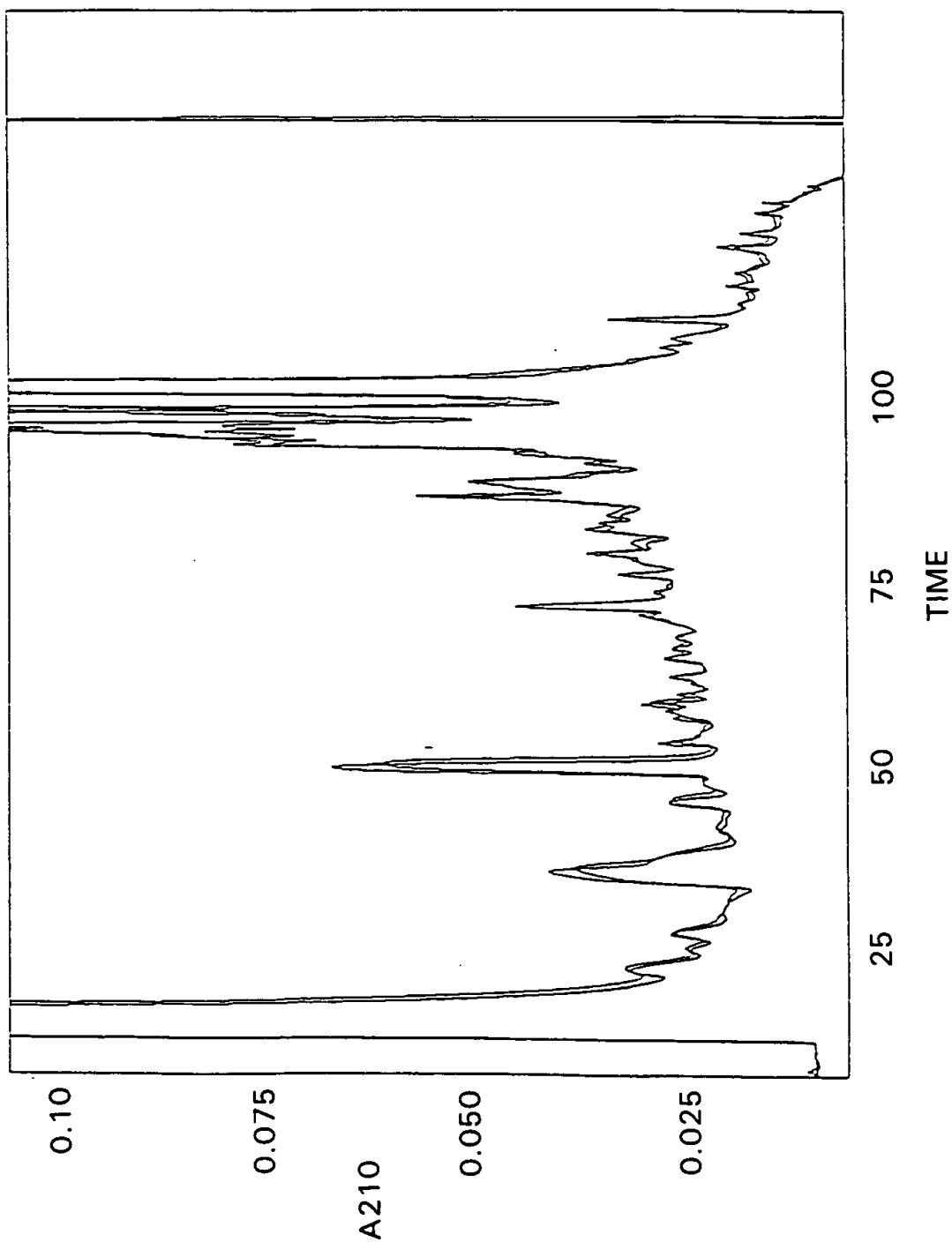
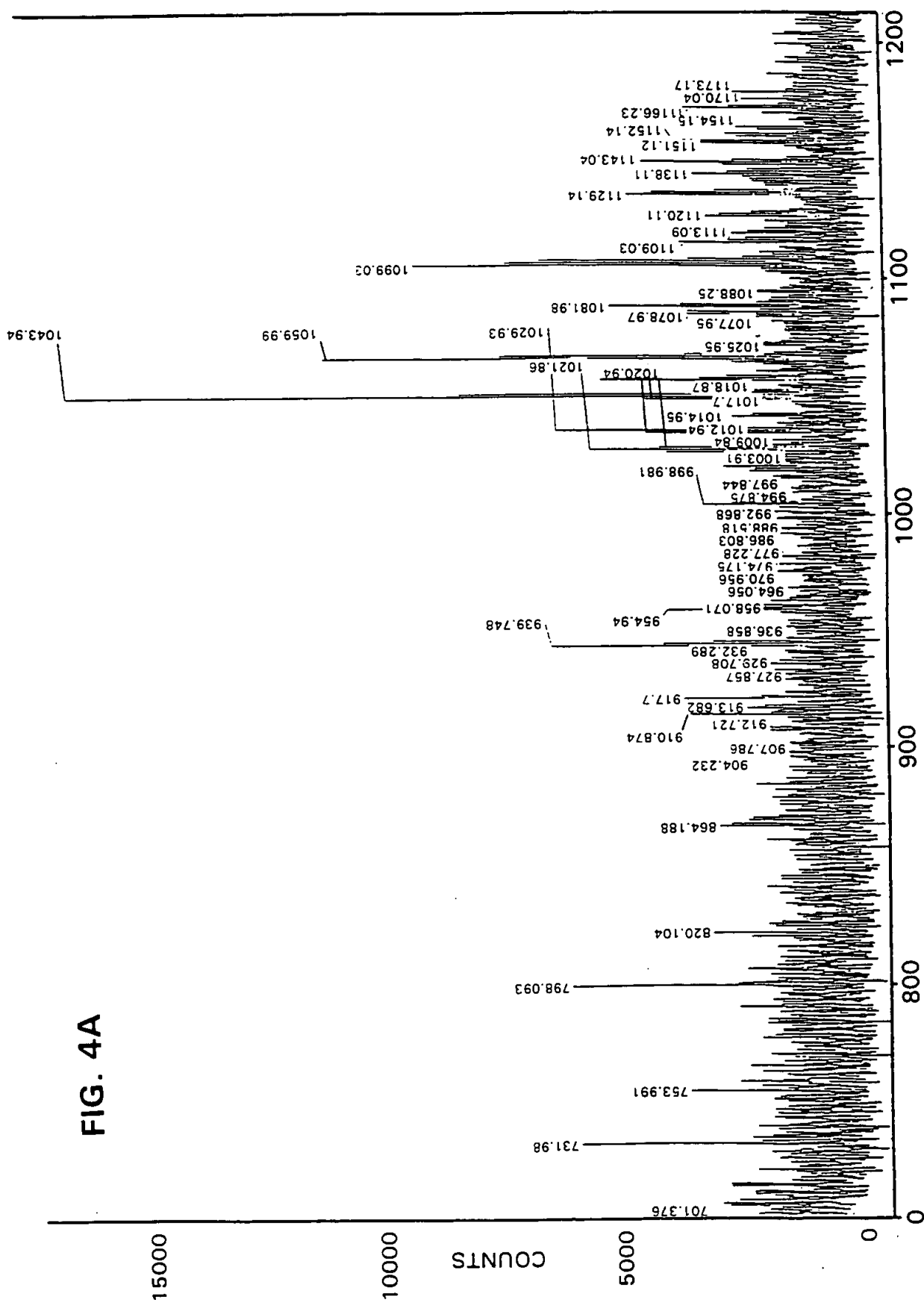


FIG. 2



**FIG. 3**



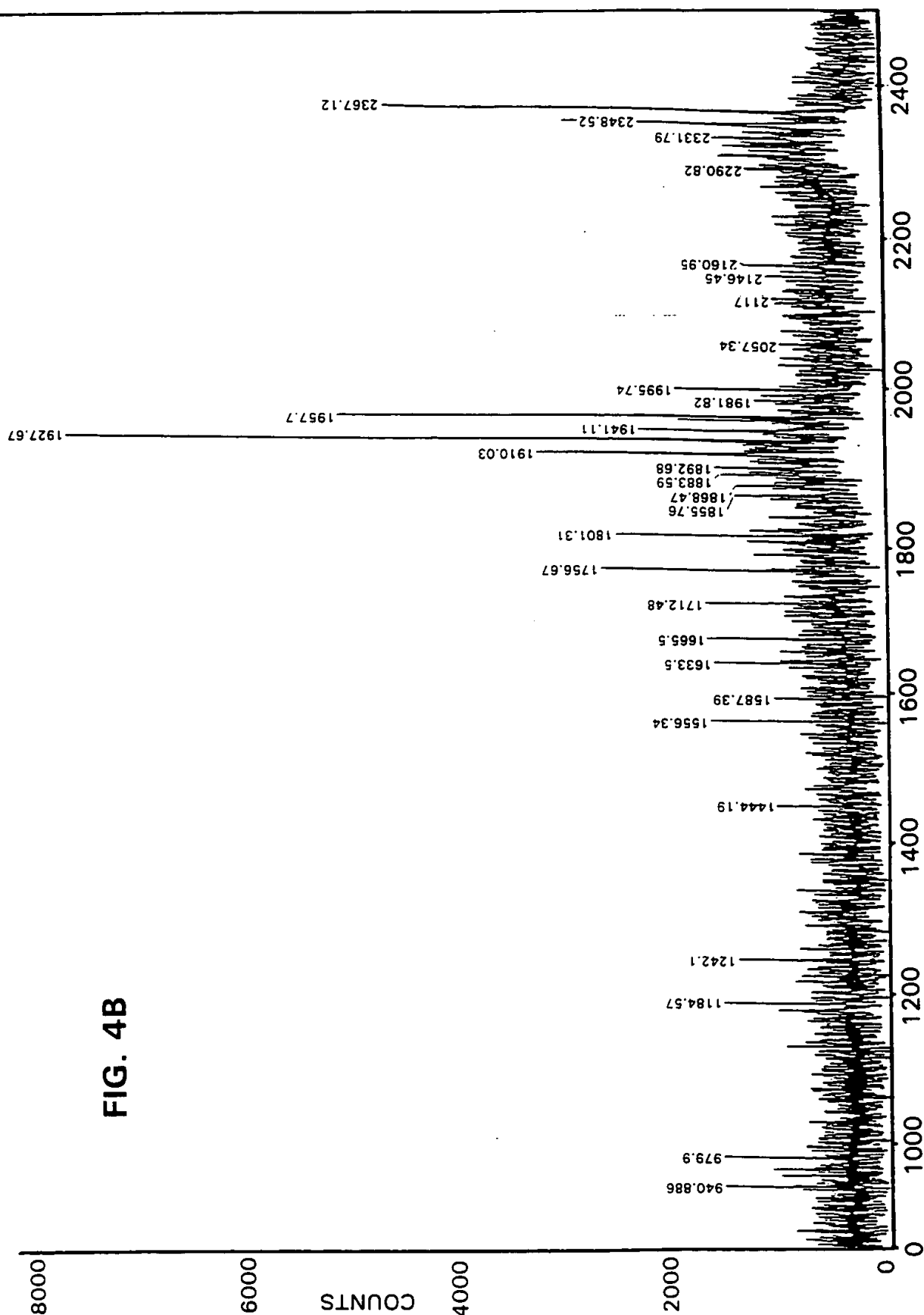
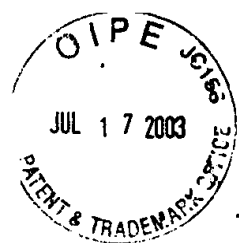
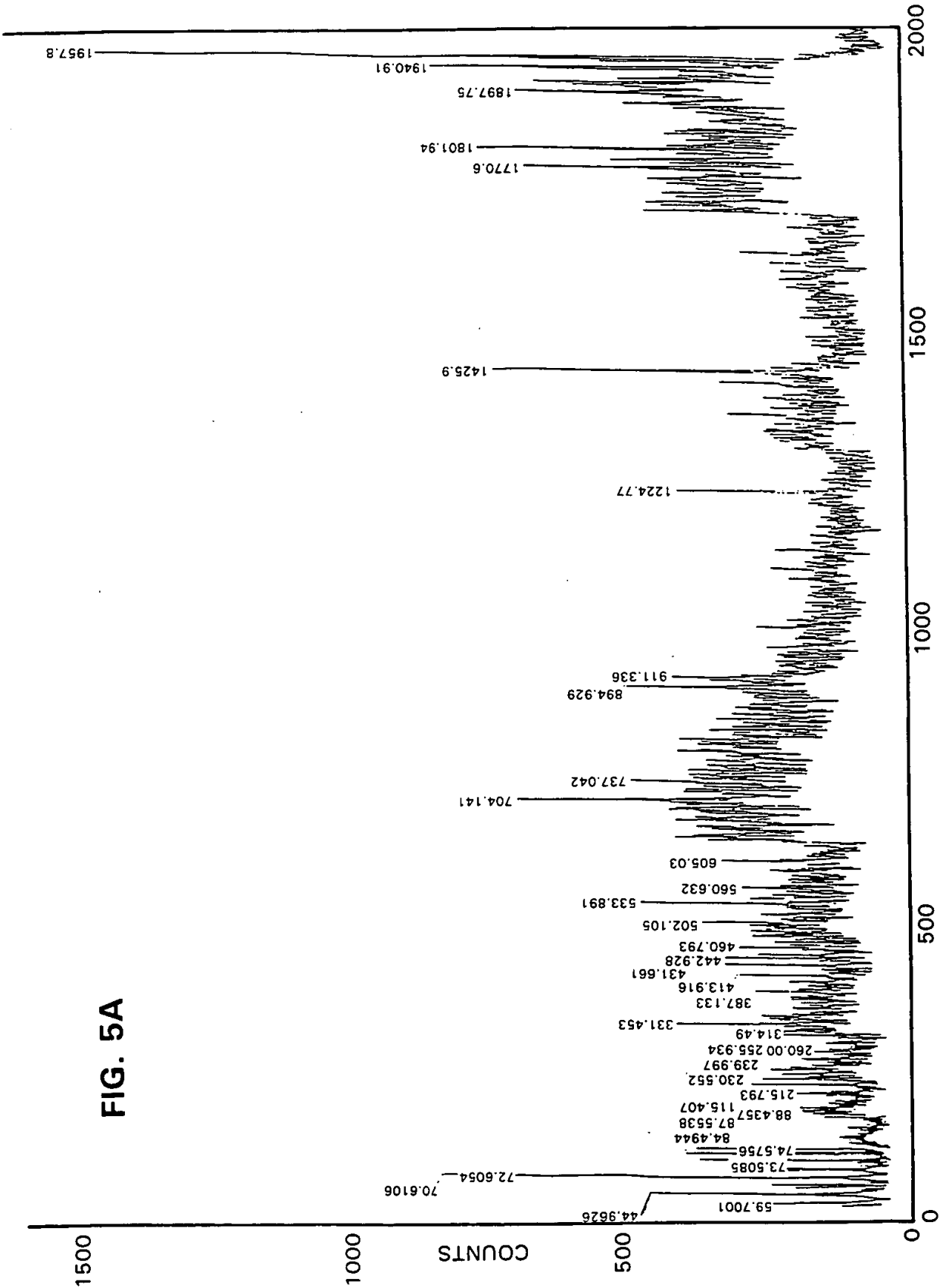




FIG. 5A





Sample ID (comment): R4A3F37m1957  
Database searched: NCBIhr.7.5.97  
Molecular weight search (1000-100000 Da) selects 269572 entries.  
Species search (HOMO SAPIENS) selects 22771 entries.  
Combined molecular weight and species searches select 20933 entries.  
Number of sequences passing through parent mass filter: 84015  
search selects 257 entries  
Ion Types Considered: a b B y n h l

| Result Summary                           |                       |                                    |                 |                         |                                  |                                 |                                    |                  |  |
|--|-----------------------|------------------------------------|-----------------|-------------------------|----------------------------------|---------------------------------|------------------------------------|------------------|--|
| Search Mode                              | Max. # Unmatched Ions | Peptide Masses are Par(ml)Frag(av) | Digest Used     | Max. # Missed Cleavages | Cysteines Modified by unmodified | Peptide N terminus Hydrogen (H) | Peptide C terminus Free Acid (O H) | Unmatched Ions   | Protein Name                                     |
| Identity                                 | 5                     |                                    | No enzyme       | 1                       |                                  |                                 |                                    |                  |  |
| Parent mass: 1957.2000 (+/-500.0000ppm)  |                       |                                    |                 |                         |                                  |                                 |                                    |                  |  |
| Fragment Ions present: [RP]V[NR][KQ]FSDR |                       |                                    |                 |                         |                                  |                                 |                                    |                  |  |
| Rank                                     | MS-Digest Index#      | NCBIhr.7.597 Accession#            | Protein MW (Da) | Species                 | Calculated MH+ (Da)              | MH+ Error (Da)                  | Sequence                           | # Unmatched Ions |  |
| 1  | 240839                | 1839795                            | 21251.4         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (D82930) HLA-A26-variant                         |
| 1  | 152874                | 915219                             | 40679.8         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (U25971) MHC class 1 antigen HLA-A2407           |
| 1  | 141923                | 825673                             | 20921.2         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (X82161) HLA-A alpha1 and alpha2 domains         |
| 1  | 159176                | 994765                             | 41113.1         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (D32129) HLA-A26                                 |
| 1  | 282322                | 250934                             | 38703.4         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (Z97370) human leukocyte antigen                 |
| 1  | 133479                | 717123                             | 40895.1         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (U18930)MHC class 1 antigen HLA-A2               |
| 1  | 49436                 | 785055                             | 38355.8         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (M160010) HLA-AH class 1 antigen (AA at 30)      |
| 1  | 277806                | 2394324                            | 10423.4         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (AF017310) MHC class 1 antigen                   |
| 1  | 277805                | 2394322                            | 10430.3         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (AF017309) MHC class 1 antigen                   |
| 1  | 277713                | 2394009                            | 21027.3         | HOMO SAPIENS            | 1956.9052                        | 0.2948                          | (Y)VDDTQFVRFDSDAASQR(M)            | 2                | (AF012767) MHC class 1 antigen HLA-A heavy chain |

FIG. 5B





gb/AA548636/AA548636.nj.38d02.s1.NCI.CCAP.AA1.Homo.Sapiens.cDNA.clone  
IMAGE.994755.similar.to.gb:z46633.HLA.CLASS.I.HISTOCOMPATIBILITY  
ANTIGEN,A-2.a\*0201.ALPHA.(HUMAN);  
Length = 539

Plus Strand HSPs:

Score = 30 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 152 VDDTQFVRFSDAASQRM 205

gb/AA147151/AA147151.zo32d06.r1.Stratagene.colon.(#937204).Homo.sapiens  
cDNA.clone.5885875.similar.to.gb:M64740.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,A-24.(A-9).A\*2402.ALPHA.(HUMAN);  
Length = 581

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
13 VDDTQFVRFSDAASQRM 66

gb/H23377/H23377.yf57e02.r1.Homo.sapiens.cDNA.clone.52227.5'similar.to  
gb:x00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3A.A\*0301  
ALPHA.(HUMAN);  
Length = 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 154 VDDTQFVRFSDAASQRM 207

gb/R13904/R13904.yf62c03.r1.Homo.sapiens.cDNA.clone.26801.5'similar.to  
gb:m64742.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-23(A-9)  
A\*2301.(HUMAN);  
Length = 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 146 VDDTQFVRFSDAASQRM 199

gb/R12066/R12066.yf54d10.r1.Homo.sapiens.cDNA.clone.26062.5'similar.to  
gb:x00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3A\*0301  
alpha.(human);  
Length = 405

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 9.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 158 VDDTQFVRFSDAASQRM 211

gb/AA132653/AA132653.zo21a05.r1.Stratagene.colon.(#937204).Homo.sapiens  
cDNA.clone.587504.5'similar.to.gb:z46633.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,A-2.A\*0201.ALPHA.(HUMAN);  
Length = 428

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 158 VDDTQFVRFSDAASQRM 203

gb/R59764/R59764.yh07c05.r1.Homo.sapiens.cDNA.clone.42563.5'similar.to  
gb:x00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3.A\*0301  
ALPHA.(HUMAN);  
Length = 461

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
138 VDDTQFVRFSDAASQRM 210

gb/AA489534/AA489534.ab37f08.r1.Stratagene.HeLa.cell.s3.937216.Homo  
sapiens.cDNA.clone.843015.5'similar.to.gb:L06425.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,AW-34(A-10).A\*3402.ALPHA.(HUMAN);  
Length = 478

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFSDAASQRM 18  
VDDTQFVRFSDAASQRM  
Sbjct: 138 VDDTQFVRFSDAASQRM 191

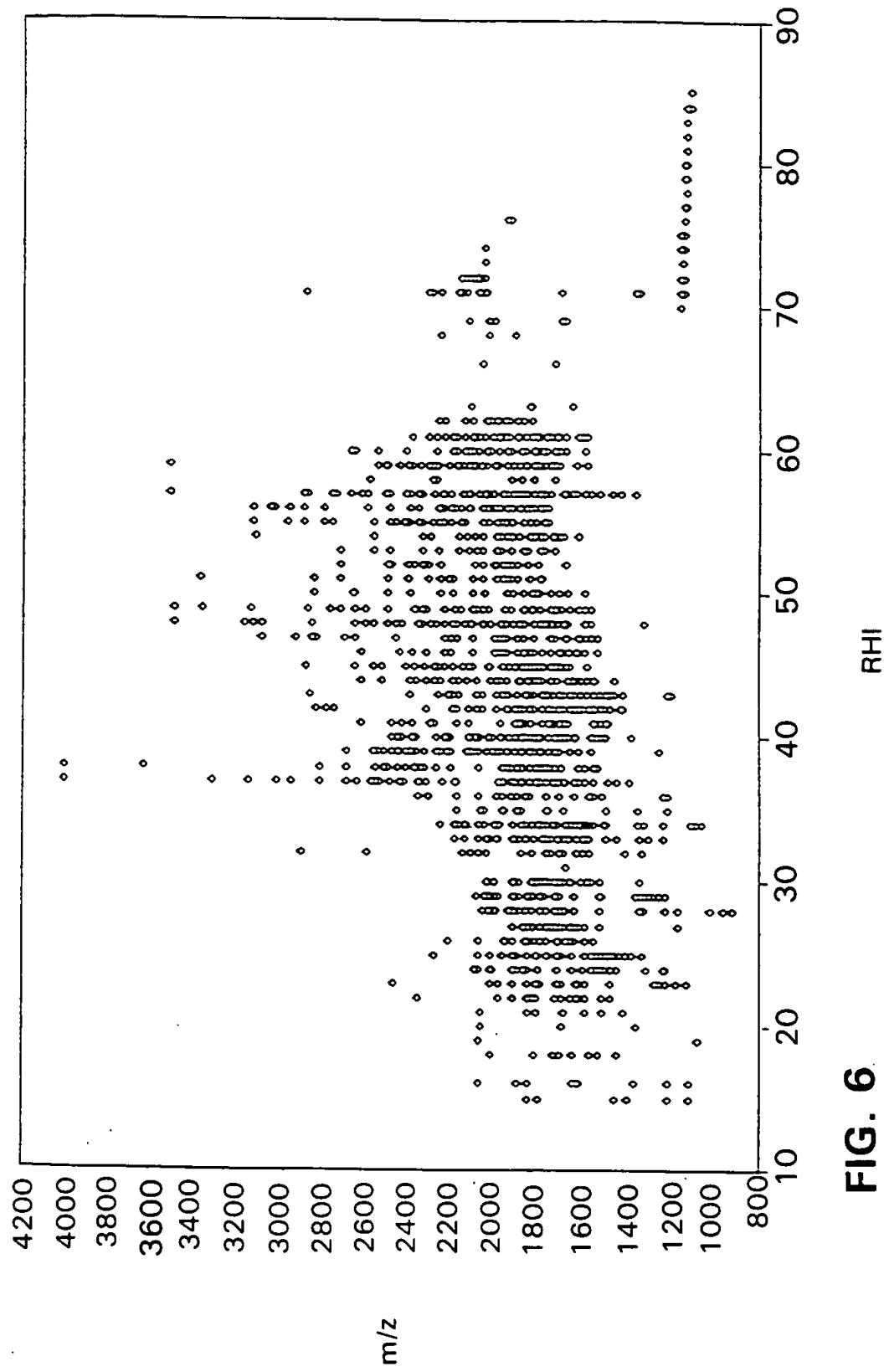


FIG. 6